

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Oct 5 10:51:34 1998; MasPar time 16.33 Seconds
587.549 Million cell updates/sec

Tabular output not generated.

Title: >US-08-908-884-3
Description: (1-593) from US08908884.pep
Perfect Score: 4122
Sequence: 1 MDTTIDGFADSYEISSTSFV..... STSKSTGGKRSNRKLSHRRR 593

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 36.233; Variance 181.818; scale 0.199

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%					
No.	Score	Match	Length	DB	ID	Description	Pred. No.

1	4122	100.0	593	29	W23963	Arabidopsis thaliana	0.00e+00
2	180	4.4	991	16	R80096	Black widow spider de	1.80e-04
3	180	4.4	1214	16	R80097	Black widow spider de	1.80e-04
4	125	3.0	679	14	R82661	Partial murine 2-5A-d	1.17e+00
5	125	3.0	679	21	W12703	Mouse 2-5A-dependent	1.17e+00
6	125	3.0	679	11	R59077	2-5A-dependent RNA-as	1.17e+00
7	123	3.0	741	14	R82660	Human 2-5A-dependent	1.58e+00
8	123	3.0	741	11	R59076	2-5A-dependent RNA-as	1.58e+00
9	123	3.0	741	14	R82659	Human 2-5A-dependent	1.58e+00
10	123	3.0	741	21	W12702	Human 2-5A-dependent	1.58e+00
11	115	2.8	339	17	R89748	AFT-1 interacting pro	5.24e+00
12	113	2.7	226	21	W15483	Human P28.	7.04e+00
13	110	2.7	718	22	W01537	Bovine ribonuclease L	1.09e+01
14	106	2.6	281	19	W02622	Yeast GCN4 transcript	1.95e+01
15	108	2.6	381	21	W15462	Haemangioma factor-1.	1.46e+01
16	107	2.6	587	8	R41889	Thermostable pyruvic	1.69e+01
17	108	2.6	1078	6	R28963	Notch hN3k full lengt	1.46e+01
18	104	2.5	281	21	W13955	LZ variant of GCN4.	2.60e+01
19	103	2.5	403	22	W11218	Leishmania braziliens	3.00e+01
20	102	2.5	403	23	W24290	LbeIF4A.	3.45e+01
21	102	2.5	403	15	R77503	Leishmania sp. antige	3.45e+01
22	102	2.5	403	23	W24291	LmeIF4A.	3.45e+01
23	103	2.5	422	11	R58599	Fowlpox virus protein	3.00e+01
24	103	2.5	422	11	R58855	Fowlpox virus (FPV) g	3.00e+01
25	103	2.5	422	21	W10693	Homology vector 443-8	3.00e+01
26	102	2.5	440	17	R94600	S4 protein.	3.45e+01
27	101	2.5	752	17	R83018	Calcium-independent c	3.98e+01
28	101	2.5	752	22	W17849	Hamster cytosolic pho	3.98e+01
29	101	2.5	752	20	W01479	Calcium-independent c	3.98e+01
30	101	2.5	752	21	W13163	Ca-independent phosph	3.98e+01
31	99	2.4	260	15	R85485	Murine CD40 ligand.	5.28e+01
32	98	2.4	260	7	R36702	Murine CD40-L.	6.07e+01
33	97	2.4	260	28	W41179	CD40 ligand.	6.98e+01
34	97	2.4	260	10	R53970	Mouse CD40-L type II	6.98e+01
35	97	2.4	281	19	W02621	Yeast GCN4 transcript	6.98e+01
36	98	2.4	293	13	R74644	Smallpox virus strain	6.07e+01
37	97	2.4	317	6	R29577	IkB NF-kappa-B-bindin	6.98e+01
38	100	2.4	365	1	P91461	Rpt-1 clone cDNA inse	4.58e+01
39	97	2.4	560	28	W26763	Human DNA replication	6.98e+01
40	97	2.4	732	23	W14068	Helicobacter pylori f	6.98e+01
41	98	2.4	976	29	W41377	Rat protein p138.	6.07e+01
42	98	2.4	1030	29	W41378	Human protein p164.	6.07e+01
43	99	2.4	1052	15	R88577	Mouse focal adhesion	5.28e+01
44	98	2.4	1052	15	R88576	Human focal adhesion	6.07e+01
45	99	2.4	2185	2	R12141	Enteroviral polypepti	5.28e+01

ALIGNMENTS

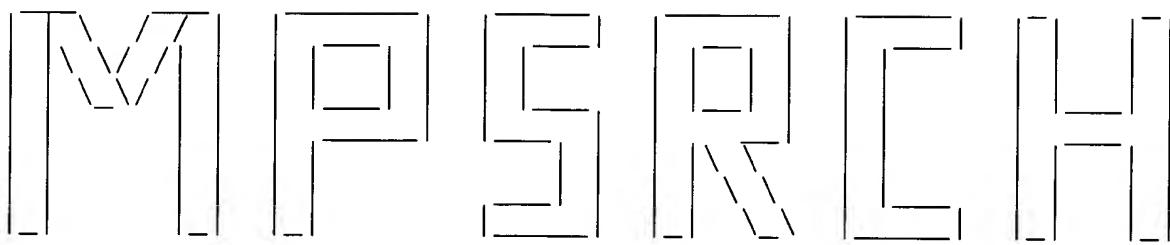
RESULT 1
ID W23963 standard; Protein; 593 AA.
AC W23963;
DT 17-JUN-1998 (first entry)

DE Arabidopsis thaliana NIM1 protein.
KW NIM1; noninducible immunity; disease resistance; plants;
KW SAR gene expression.
OS Arabidopsis thaliana.
PN WO9749822-A1.
PD 31-DEC-1997.
PF 10-MAR-1997; E01218.
PR 10-JAN-1997; US-035022.
PR 21-JUN-1996; US-020272.
PR 30-AUG-1996; US-024883.
PR 13-DEC-1996; US-033177.
PR 27-DEC-1996; US-773559.
PA (NOVS) NOVARTIS AG.
PI Delaney TP, Ellis DM, Friedrich LB, Johnson JE,
PI Lawton KA, Ryals JA, Weymann K;
DR WPI; 98-077185/07.
DR N-PSDB; V04632.
PT NIM1 gene which allows activation in plant of systemic acquired
PT resistance - useful to confer broad spectrum disease resistance in
PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and
PT corn
PS Disclosure; Fig 15; 153pp; English.
CC The sequence is that of the NIM1 (noninducible immunity) protein. It
CC may be used to confer a broad spectrum disease resistance in plants,
CC specifically crop plants, e.g. rice, wheat, barley, rye and corn.
CC The NIM1 gene can be used to confer universal disease susceptibility
CC to plant cells, and their progeny. It can also be used in a screening
CC method for identifying compounds capable of inducing broad spectrum
CC disease resistance in plants, while the plant cells, and their
CC progeny, can be used to isolate a gene fragment which allows
CC expression of broad spectrum disease resistance in plants, or to
CC incorporate the resistant trait into plant lines through breeding.
SQ Sequence 593 AA;

Query Match 100.0%; Score 4122; DB 29; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mdttidgfadsyeisstsfvatdntdssivylaaeqvltgpdvsalqlsnsfesvfdsp 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1 MDTTIDGFADSYEISSTSFVATDNTDSSIVYLAEEQVLTGPDVSALQLLSNSFESVFDSP 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ddfyasdaklvlsdgrevsfhrcvlsarssffksalaaakkedsnnntaavklekeakd 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 DDFYSDAKLVLSDGREVSFHRcvLSARSSFFKSALAAAKKEKDSNNNTAAVKLELKEAKD 120
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Db 121 yevgfdsvvttvlayvyssrvrpppkvgvsecadencchvacrpavdfmlevlyafifkip 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 YEVGFDSVVTVLAYVYSSRVRPPPKGVSECADENCCHVACRPAVDFMLEVLYAFIFKIP 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 elitlyqrh1ldvvdkvviedtlvilklanicgkacmk1ldrckeivksnvdmsleks 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 ELITLYQRHLLDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIVKSNVDMVSLEKS 240

Db	241	lpeelvkeiidrrkelglevpkvvkhvsnvhkal	dsddielvkllkedhtnlddacalh	300				
Qy	241	LPEELVKEIIDRRKELGLEVPKVKHVSNVHKAL	DSDDIELVKLLKEDHTNLDDACALH	300				
Db	301	favaycnvktatdllkldladvnhrnprgytv	lhvaamrkepqlilsllekgasaseat	360				
Qy	301	FAVAYCNVKTATDLLKLDLADVNH	RNPRGYTVLHVAAMRKEPQLILSLEKGASASEATL	360				
Db	361	egrtalmiakqatmavecnnipeqckhs1kgrl	cveileqedkreqiprdvppsfavaad	420				
Qy	361	EGRTALMIAKQATMAVECNNIPEQCKHSLKGRL	CVEILEQEDKREQIPRDVPPSFAVAAD	420				
Db	421	elkmtlldlenrvalaqrlfp	teaqaaameiaemkgtcefivtslepdr	ltgtkrtspgvk	480			
Qy	421	ELKMTLLDLENRVALAQR	LFPTEAQAAAMEIAEMKGTCEFIVTSL	EPDRLTGTKRTSPGVK	480			
Db	481	ia	pfrileehqsrlkalsktvelgkrffprcsav	ldqimncedltqlacgeddt	taekrlq	540		
Qy	481	IAPFRILEEHQSRLKALS	KTVELGKRFFPRCSAVLDQIMNCEDLT	QLACGEDDTAEKRLQ	540			
Db	541	kkqrymeiqetlk	kafsednlelg	nnsslt	dstssts	skstggkrsnrklshrrr	593	
Qy	541	KKQRYMEIQETLK	KAFSEDNLELG	NNSSLTD	STS	SKSTGGKRSNRKL	SHRRR	593



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Oct 5 20:40:04 1998; MasPar time 2645.00 Seconds
1508.451 Million cell updates/sec
Tabular output not generated.

Title: >US-08-908-884-13
Description: (1-2172) from US08908884.seq
Perfect Score: 2172
N.A. Sequence: 1 GTGACTTTCTAACTATGGCT.....ATTTGAAAAA..... 2172
Comp: CACTGAAAGATTGATACCGA.....TAAACTTTTTTTTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 532259 seqs, 918475165 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl155
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro

Database: genbank107
12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat
18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st
24:gb_sts 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 11.830; Variance 6.147; scale 1.925

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query		Length	DB	ID	Description	Pred.	No.
			Match	%						
	1	328	15.1	2104	19	ATU76707		Arabidopsis thaliana r	1.27e-228	
	2	165	7.6	5655	19	ATU87794		Arabidopsis thaliana t	7.33e-99	
	3	74	3.4	7218	17	I66494		Sequence 14 from paten	2.44e-30	
c	4	68	3.1	7218	17	I66494		Sequence 14 from paten	4.07e-26	
	5	40	1.8	10772	14	AF012089		Drosophila melanogaste	1.15e-07	
c	6	37	1.7	10772	14	AF012089		Drosophila melanogaste	6.99e-06	
	7	34	1.6	354	14	OFU89259		Oxytricha fallax 57kD	3.70e-04	
	8	33	1.5	215	17	I28278		Sequence 5 from patent	1.34e-03	
c	9	33	1.5	103548	13	HS292E10		Human DNA sequence ***	1.34e-03	
	10	32	1.5	152580	13	HS366L4		Human DNA sequence ***	4.79e-03	
c	11	28	1.3	375	24	G25545		human STS EST118797.	6.22e-01	
c	12	28	1.3	529	24	G27780		human STS SHGC-33252.	6.22e-01	
	13	28	1.3	125536	13	AC003021		*** SEQUENCING IN PROG	6.22e-01	
c	14	28	1.3	168133	13	HS500L14		Human DNA sequence ***	6.22e-01	
	15	28	1.3	219090	13	HS212A2		Human DNA sequence ***	6.22e-01	
c	16	26	1.2	30	9	A62994		Sequence 6 from Patent	6.11e+00	
c	17	26	1.2	60	9	A62989		Sequence 1 from Patent	6.11e+00	
	18	25	1.2	111	9	A60119		Sequence 7 from Patent	1.83e+01	
c	19	26	1.2	215	17	I28278		Sequence 5 from patent	6.11e+00	
	20	25	1.2	267	24	BLYBD		Hordeum vulgare (clone	1.83e+01	
	21	25	1.2	400	24	G10880		human STS SHGC-9303 cl	1.83e+01	
c	22	26	1.2	565	17	E04076		gDNA encoding envelope	6.11e+00	
c	23	27	1.2	602	24	HUMUT6251		Human STS UT6251.	1.98e+00	
	24	26	1.2	818	19	BOU93838		Blechnum occidentale A	6.11e+00	
c	25	25	1.2	1122	14	AF020286		Dictyostelium discoide	1.83e+01	
	26	26	1.2	1416	19	LUU59284		Linum usitatissimum pe	6.11e+00	
	27	25	1.2	1577	19	DDINDKM		Dictyostelium discoide	1.83e+01	
	28	26	1.2	1918	14	S72639		PspB=prespore-specific	6.11e+00	
c	29	25	1.2	2222	14	DDSP96A		Dictyostelium discoide	1.83e+01	
	30	25	1.2	2493	20	HUMIGHAD		Human Ig rearranged H-	1.83e+01	
c	31	25	1.2	2904	21	HSAC001456		Homo sapiens (subclone	1.83e+01	
	32	25	1.2	8042	21	HSHCFC1		H.sapiens HCFC1 gene.	1.83e+01	
	33	26	1.2	9705	19	CHLC27		C.ellipsoidea rbcL, rp	6.11e+00	
	34	25	1.2	27119	14	CEF08B12		Caenorhabditis elegans	1.83e+01	
c	35	25	1.2	40977	21	HSAC000362		Human cosmid g1346a094	1.83e+01	
c	36	25	1.2	41702	21	HSAC000366		Human cosmid g1862x046	1.83e+01	
	37	26	1.2	78794	21	AC003990		Human BAC clone RG035M	6.11e+00	
c	38	25	1.2	116019	21	AC004629		Homo sapiens chromosom	1.83e+01	
c	39	26	1.2	120007	21	AF064864		Homo sapiens chromosom	6.11e+00	
c	40	26	1.2	133469	13	HSAC000383		*** SEQUENCING IN PROG	6.11e+00	
	41	25	1.2	145717	13	HS108K11		Human DNA sequence ***	1.83e+01	
	42	26	1.2	150613	19	AB001684		Chlorella vulgaris C-2	6.11e+00	
	43	25	1.2	156601	21	HS212G6		Homo sapiens DNA seque	1.83e+01	
	44	25	1.2	160000	13	AC004062		*** SEQUENCING IN PROG	1.83e+01	
c	45	25	1.2	224036	13	AC004787		*** SEQUENCING IN PROG	1.83e+01	

ALIGNMENTS

LOCUS ATU76707 2104 bp mRNA PLN 14-JAN-1997
 DEFINITION Arabidopsis thaliana regulatory protein NPR1 (NPR1) mRNA, complete
 cds.
 ACCESSION U76707
 NID g1773294
 KEYWORDS .
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
 Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2104)
 REFERENCE AUTHORS Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.
 TITLE The Arabidopsis NPR1 gene that controls systemic acquired
 resistance encodes a novel protein containing ankyrin repeats
 JOURNAL Cell 88 (1), 57-63 (1997)
 MEDLINE 97148688
 2 (bases 1 to 2104)
 REFERENCE AUTHORS Cao,H., Glazebrook,J., Clarke,J.D., Volko,S. and Dong,X.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC
 Building, Research Dr., Durham, NC 27708-1000, USA
 FEATURES source Location/Qualifiers
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 RPAVDFMLEVLYLAFIFKIPELITLYQRHLLDVVDKVVIEDTLVILKLANICGKACMK
 LLDRCKEIIVKSNVDMVSLEKSLPEELVKEIIDRRKELGLEVPKVKKHVSNVHKALDS
 DDIELVKLLLKEDHTNLDDACALHFAYCNVKTATDLLKLDLADVNHRNPRGYTVLH
 VAAMRKEPQLLISLLEKGASASEATLEGRTALMIAKQATMAVECNNIPEQCKHSLKGR
 LCVEILEQEDKREQIPRDVPPSFAVAADELKMTLLDLENRVALAQRILFPTEAQAAMEI
 AEMKGTCFIVTSLEPDRLTGTKRTSPGVKIAPFRILEEHQSRLKALSKTVELGKRRF
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 BASE COUNT 606 a 431 c 482 g 585 t
 ORIGIN

Query Match 15.1%; Score 328; DB 19; Length 2104;
 Best Local Similarity 64.8%; Pred. No. 1.27e-228;

Matches 882; Conservative 0; Mismatches 464; Indels 15; Gaps 5;

Db	423	AAGCTCGAGCTTAAGGAGATTGCCAAGGATTACGAAGTCGGTTCGATTCGGTTGTGACT	482
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Db	483	GTGTTGGCTTATGTTACAGCAGCAGAGTGAGACCGCCGCCTAAAGGAGTTCTGAATGC	542
Qy	615	GTATTGGCTTATTGTATAGTGGTAAAGTTAGGCCTTCACCTAAAGATGTGTGTGTTGT	674
Db	543	GCAGACGAGAATTGCTGCCACGTGGCTGCCGGCGCGGTGGATTTCATGTTGGAGGTT	602
Qy	675	GTGGACAATGACTGCTCTCATGTGGCTTGAGGCCAGCTGTGGCATTCTGGTTGAGGTT	734
Db	603	CTCTATTTGGCTTCATCTCAAGATCCCTGAATTAAATTACTCTCTATCAGAGGCACCTA	662
Qy	735	TTGTACACATCATTACCTTCAGATCTCTGAATTGGTTGACAAGTTCAAGAGACACCTA	794
Db	663	TTGGACGTTGAGACAAAGTTGTTATAGAGGACACATTGGTTATACTCAAGCTTGCTAAT	722
Qy	795	CTGGATATTCTTGACAAAAGTGCAGCAGACGATGTAATGATGGTTTATCTGTTGCAAAC	854
Db	723	ATATGTGGTAAAGCTTGTATGAAGCTATTGGATAGATGAAAGAGATTATTGTCAAGTCT	782
Qy	855	ATTTGTGGTAAAGCATGCGAGAGATTGCTTCAAGCTGCATTGAGATTATTGTCAAGTCT	914
Db	783	AATGTAGATATGGTTAGTCTTGAAGGCTATTGCCGGAAGAGCTTGTAAAGAGATAATT	842
Qy	915	AATGTTGATATCATAACCCTTGATAAAGCCTTGCTCATGACATTGAAACAAATTACT	974
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Qy	975	GATTACGAGCGGAACCTGGCTACAAGGGCCTGAAAGCAACGGTTTCCTGATAAACAT	1034
Db	891	GTCTCGAATGTACATAAGGCACTTGACTCGGATGATATTGAGTTAGTCAGTTGCTTTG	950
Qy	1035	GTAAAGAGGATACATAGGGCATTGGATTCTGATGATGTTGAATTACTACAAATGTTGCTA	1094
Db	951	AAAGAGGATCACACCAATCTAGATGATGCGTGTGCTCTCATTGCTGTTGCATATTGC	1010
Qy	1095	AGAGAGGGCATACTACCCTAGATGATGCATATGCTCTCATTATGCTGTAGCGTATTGC	1154
Db	1011	AATGTGAAGACCGAACAGATCTTTAAAACCTGATCTGCCGATGTCAACCATAAGGAAT	1070
Qy	1155	GATGCAAAGACTACAGCAGAACTTCTAGATCTGCACCTGCTGATATTAATCATCAAAT	1214
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Qy	1215	TCAAGGGATACACGGTCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAATTGTAGTG	1274
Db	1131	TCTCTATTGGAAAAAGGTGCAAGTGCATCAGAACCAACTTGGAAAGGTAGAACCGCACTC	1190
Qy	1275	TCCCTTTAACCAAAGGAGCTAGACCTCTGATCTGACATCCGATGGAAGAAAAGCACTT	1334

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Qy 1335 CAAATCGCCAAGAGGCTCACTAGGCTTGTGGATTCAAGTCTCCGGAGGAAGGAAAA 1394

Db 1251 CATTCTCTCAAAGGCCACTATGTGTAGAAATACTAGAGCAAGAAGACAAACGAGAACAA 1310
Qy 1395 TCTGCTTCGAATGATCGGTTATGCATTGAGATTCTGGAGCAAGCAGAAAGAAGAGACCT 1454

Db 1311 ATTCCCTAGAGATGTTCCCTCCCTTTGCAGTGGCGGCCGATGAATTGAAGATGACGCTG 1370
Qy 1455 CTGCTAGGAGAAGCTCTGTATCTCTGCTATGGCAGGCGATGATTGCGTATGAAGCTG 1514

Db 1371 CTCGATCTTGAAAATAGAGTTGCACTTGCTAACGTCTTTCCAACGGAAGCACAAGCT 1430
Qy 1515 TTATACCTTGAAAATAGAGTTGGCCTGGCTAAACTCCTTTCCAATGGAAGCTAAAGTT 1574

Db 1431 GCAATGGAGATCGCCGAAATGAAGGGAACATGTGAGTTCATAGTGACTIONCCTCGAGCCT 1490
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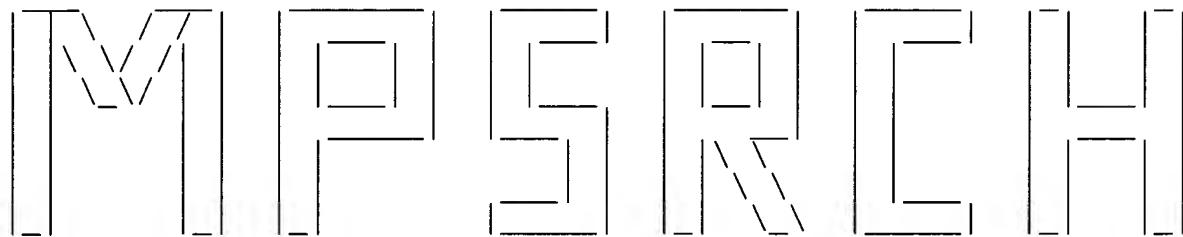
Db 1491 GACCGTCTCACTGGTACGAAGAGAACATCACCGGGTGTAAAGATAGCACCTTCAGAAC 1550
Qy 1634 AAA-GA-TGGCTAATGCACAGAGGACAACAGTAGATTGAAACGAGGCTCCTTCAAGATA 1691

Db 1551 CTAGAAGAGCATCAAAGTAGACTAAAAGCGCTTCTAAAACCGTGGAACTCGGGAAACGA 1610
Qy 1692 AAAGAGGAGCACTTGAATCGGCTTAGAGCACTCTAGAACTGTAGAACTTGGAAAACGC 1751

Db 1611 TTCTTCCCGCGCTGTTGGCAGTGCTCGACCAGATTATGAACTGTGAGGACTTGACTCAA 1670
Qy 1752 TTCTTCCACGTTGTTAGAAAGTTCTAAATAAGATCATGGATGCTGATGACTTGTCTGAG 1811

Db 1671 CTGGCTTGCAGAGAACGACACTGCTGAGAAACGACTACAAAAGAAGCAAAGGTACATG 1730
Qy 1812 ATAGCTTACATGGGAATGATAACGGCAGAAGAGCGTCAACTGAAGAAGCAAAGGTACATG 1871

Db 1731 GAAATACAAGAGACACTAAAGAAGGCCTTAGTGAGGACAA 1771
Qy 1872 GAACTCAAGAAATTCTGACTAAAGCATTCACTGAGGATAA 1912



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Mon Oct 5 22:08:16 1998; MasPar time 313.34 Seconds
 943.086 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-908-884-13
 Description: (1-2172) from US08908884.seq
 Perfect Score: 2172
 N.A. Sequence: 1 GTGACTTCTAACTATGGCT.....ATTGAAAAAAAAAAAAAA 2172
 Comp: CACTGAAAGATTGATACCGA.....TAAACTTTTTTTTTTTTT
 Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40

Statistics: Mean 9.671; Variance 6.087; scale 1.589

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES								
Result	Query				Description			Pred. No.
	No.	Score	Match	Length	DB	ID		
c 1	165	7.6	5655	40	V04632	Arabidopsis thaliana	1.35e-85	
c 2	165	7.6	9919	40	V04631	Arabidopsis thaliana	1.35e-85	
c 3	43	2.0	204	1	N81164	Base substituted E.co	9.86e-10	
4	40	1.8	91	9	Q51746	Oligonucleotide probe	4.18e-08	
5	39	1.8	204	1	N81164	Base substituted E.co	1.43e-07	
c 6	38	1.7	91	9	Q51746	Oligonucleotide probe	4.87e-07	
7	35	1.6	114	12	Q70467	Generic DNA sequence	1.80e-05	
8	34	1.6	114	12	Q70469	Generic DNA sequence	5.87e-05	
9	34	1.6	114	12	Q70465	Generic DNA sequence	5.87e-05	
c 10	35	1.6	114	12	Q70465	Generic DNA sequence	1.80e-05	
c 11	34	1.6	114	12	Q70468	Generic DNA sequence	5.87e-05	

C	12	34	1.6	114	12	Q70466	Generic DNA sequence	5.87e-05
	13	32	1.5	114	12	Q70468	Generic DNA sequence	6.02e-04
C	14	32	1.5	114	12	Q70467	Generic DNA sequence	6.02e-04
	15	32	1.5	501	3	N50024	Sequence encoding new	6.02e-04
	16	32	1.5	501	3	N50026	Sequence encoding new	6.02e-04
	17	30	1.4	114	12	Q70466	Generic DNA sequence	5.86e-03
	18	30	1.4	114	12	Q70470	Generic DNA sequence	5.86e-03
C	19	31	1.4	114	12	Q70469	Generic DNA sequence	1.89e-03
	20	31	1.4	3871	2	N71302	HSV-1 gB and surround	1.89e-03
	21	28	1.3	39	7	Q51787	Mixed oligonucleotide	5.37e-02
C	22	29	1.3	114	12	Q70470	Generic DNA sequence	1.79e-02
C	23	28	1.3	114	12	Q70472	Generic DNA sequence	5.37e-02
	24	28	1.3	498	3	N50034	Sequence encoding new	5.37e-02
	25	29	1.3	501	3	N50030	Sequence encoding new	1.79e-02
	26	28	1.3	501	3	N50029	Sequence encoding new	5.37e-02
	27	28	1.3	501	3	N50031	Sequence encoding new	5.37e-02
	28	28	1.3	501	3	N50023	Sequence encoding new	5.37e-02
	29	28	1.3	501	3	N50028	Sequence encoding new	5.37e-02
	30	28	1.3	501	3	N50032	Sequence encoding new	5.37e-02
C	31	25	1.2	75	21	T13612	DC43 TSAR library gen	1.31e+00
	32	25	1.2	111	36	T96515	MSRV-1B general conse	1.31e+00
	33	26	1.2	114	12	Q70471	Generic DNA sequence	4.60e-01
C	34	26	1.2	114	12	Q70473	Generic DNA sequence	4.60e-01
	35	26	1.2	140	32	T76368	Human IL-8 receptor-a	4.60e-01
	36	26	1.2	172	32	T76363	Human interleukin 8 a	4.60e-01
	37	27	1.2	178	32	T76405	Human endothelin-1 an	1.59e-01
C	38	25	1.2	178	32	T76405	Human endothelin-1 an	1.31e+00
	39	27	1.2	501	3	N50025	Sequence encoding new	1.59e-01
	40	26	1.2	501	3	N50027	Sequence encoding new	4.60e-01
	41	26	1.2	501	3	N50033	Sequence encoding new	4.60e-01
C	42	25	1.2	501	3	N50026	Sequence encoding new	1.31e+00
C	43	25	1.2	501	3	N50030	Sequence encoding new	1.31e+00
C	44	25	1.2	501	3	N50032	Sequence encoding new	1.31e+00
C	45	25	1.2	501	3	N50025	Sequence encoding new	1.31e+00

ALIGNMENTS

RESULT 1

ID V04632 standard; DNA; 5655 BP.

AC V04632;

DT 17-JUN-1998 (first entry)

DE Arabidopsis thaliana NIM1 gene.

KW NIM1; noninducible immunity; disease resistance; plants;

KW SAR gene expression; ss.

OS Arabidopsis thaliana.

FH Key Location/Qualifiers

FT CDS 2787..4866)

FT /*tag= a

FT /product= "NIM1 protein"

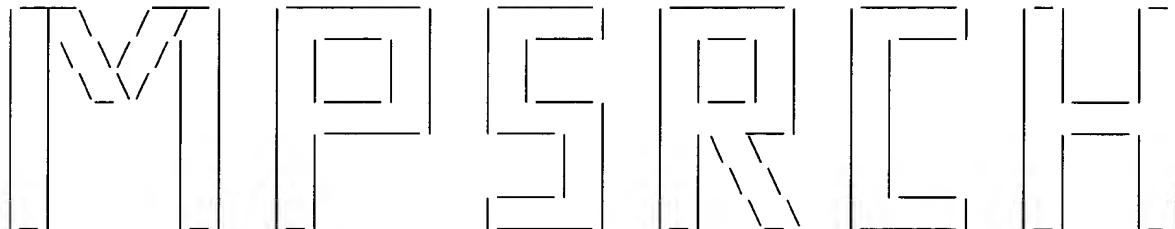
FT exon 2787..3347

FT /*tag= b

FT /number= 1

FT exon 3427..4162

Db 3838 aggaatccgaggggatatacggtgcttcatgttgcgcgcggaaaggagccacaattg 3897
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1209 CAAAATTCAAGGGGATACACGGTGCTGCATGTTGCAGCCATGAGGAAAGAGCCTAAAATT 1268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3898 atactatctctattggaaaaagggtgcgaagtgcatacagaaggcaacttggaaaggtagaacc 3957
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1269 GTAGTGTCCCTTTAACCAAAGGAGCTAGACCTCTGATCTGACATCCGATGGAAGAAAA 1328
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3958 gcactcatgatcgcaaaacaagccactatggcggttgaatgtataataatatccggagcaa 4017
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1329 GCACTTCAAATGCCAAGAGGCTCACTAGGCTTGTGGATTTCAGTAAGTCTCCGGAGGAA 1388
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4018 tgcaaggcattctctcaaaggccgactatgtgttagaaatactagagcaagaagacaaacga 4077
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1389 GGAAAATCTGCTTCGAATGATCGGTTATGCATTGAGATTCTGGAGCAAGCAGAAAGAAGA 1448
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4078 gaacaaattcttagagatgttcctccctctttgcagtggcgccatgaattgaagatg 4137
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1449 GACCCTCTGCTAGGAGAAGCTTCTGTATCTCTTGCTATGGCAGGCGATGATTGCGTATG 1508
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4138 acgctgctcgatcttggaaaatagag 4162
||| ||| ||| ||| ||| ||| ||| |||
Qy 1509 AAGCTGTTATACCTTGAAAATAGAG 1533



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Oct 5 10:54:52 1998; MasPar time 28.23 Seconds
877.191 Million cell updates/sec

Tabular output not generated.

Title: >US-08-908-884-14

Description: (1-588) from US08908884.pep

Perfect Score: 4115

Sequence: 1 MDNSRTAFSDSNDISGSSSI.....SSCSSTSKGVDKPNKLPFRK 588

Scoring table: PAM 150

Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: sptrembl6

1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal

5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant

9:sp_bacteria 10:sp_rat 11:sp_virus 12:sp_vertebrate

13:sp_unclassified

Statistics: Mean 50.515; Variance 104.765; scale 0.482

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	2184	53.1	593	8	P93002		REGULATORY PROTEIN NPR	0.00e+00
2	185	4.5	1088	2	Q13484		ANKYRIN G119.	1.55e-11
3	184	4.5	1765	10	Q61308		ANKYRIN 3.	2.21e-11
4	184	4.5	1940	10	Q61309		ANKYRIN 3.	2.21e-11
5	184	4.5	1943	10	Q61307		ANKYRIN 3, EPITHELIAL.	2.21e-11
6	184	4.5	1961	10	Q61310		ANKYRIN 3.	2.21e-11
7	185	4.5	4377	2	Q12955		ANKYRIN G.	1.55e-11
8	172	4.2	1214	3	Q25338		DELTA-LATROINSECTOTOXI	1.53e-09
9	173	4.2	1719	2	Q13768		ALT. ANKYRIN (VARIANT	1.08e-09
10	173	4.2	1856	2	Q99407		ANKYRIN.	1.08e-09
11	169	4.1	843	10	P97582		ANKYRIN (FRAGMENT).	4.33e-09
12	170	4.1	1098	10	Q61304		ERYTHROID ANKYRIN (FRA	3.06e-09
13	170	4.1	1848	10	Q61302		ERYTHROID ANKYRIN.	3.06e-09
14	147	3.6	1151	1	O13987		HYPOTHETICAL 127.7 KD	7.15e-06
15	149	3.6	1411	3	Q02989		ALPHA-LATROINSECTOTOXI	3.71e-06
16	145	3.5	1549	3	Q24241		ANKYRIN.	1.37e-05
17	139	3.4	813	3	Q24313		DNA BINDING PROTEIN.	9.41e-05
18	134	3.3	448	12	Q92010		ZINC FINGER 5 PROTEIN	4.54e-04
19	135	3.3	813	3	P90538		MIGA.	3.32e-04
20	133	3.2	449	2	O00403		ZINC FINGER 5 PROTEIN.	6.20e-04
21	133	3.2	449	10	Q08376		ZINC FINGER PROTEIN ZF	6.20e-04
22	131	3.2	1786	3	Q17344		UNC-44 (FRAGMENT).	1.15e-03
23	131	3.2	1809	3	Q17487		E. ELEGANS ANKYRIN-REL	1.15e-03
24	131	3.2	1815	3	Q17488		C. ELEGANS ANKYRIN-REL	1.15e-03
25	131	3.2	1867	3	Q17486		C. ELEGANS ANKYRIN-REL	1.15e-03
26	131	3.2	2039	3	Q17489		C. ELEGANS ANKYRIN-REL	1.15e-03
27	131	3.2	6994	3	Q17343		UNC-44 ANKYRINS.	1.15e-03
28	127	3.1	211	11	O41154		A672R PROTEIN.	3.90e-03
29	129	3.1	611	3	Q18670		HYPOTHETICAL PROTEIN C	2.12e-03
30	128	3.1	882	2	O15084		KIAA0379 (FRAGMENT).	2.88e-03
31	123	3.0	341	9	O06637		PUTATIVE FLAGELLA-RELA	1.30e-02
32	125	3.0	581	3	O16313		C05C8.6 PROTEIN.	7.13e-03
33	121	2.9	151	2	Q92527		ANKYRIN MOTIF.	2.34e-02
34	118	2.9	520	9	Q47163		(CTR5X).	5.62e-02
35	120	2.9	552	2	Q14776		LZTR-1.	3.14e-02
36	121	2.9	625	3	O18147		T27E9.4.	2.34e-02
37	120	2.9	1640	3	O17112		F39E9.2 PROTEIN.	3.14e-02
38	115	2.8	186	9	O24706		ADENYLYLATE KINASE.	1.33e-01
39	116	2.8	251	10	Q62422		SH3P2 (FRAGMENT).	1.00e-01
40	116	2.8	443	9	Q54703		EMM18.1.	1.00e-01
41	116	2.8	508	3	Q20604		F49E11.1.	1.00e-01
42	116	2.8	1005	12	O13075		NUCLEAR FACTOR NF-KB1.	1.00e-01
43	116	2.8	1401	3	Q25328		ALPHA-LATROTOXIN PRECU	1.00e-01
44	113	2.7	474	11	P87621		41KBP FRAGMENT FROM LE	2.34e-01
45	113	2.7	1001	2	Q14349		G9A PROTEIN CONTAINING	2.34e-01

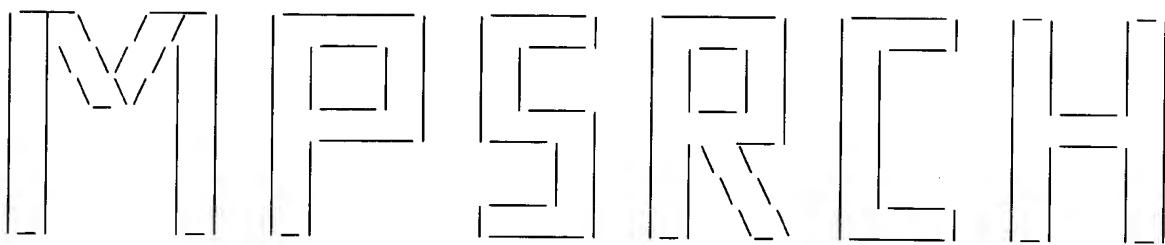
ALIGNMENTS

ID P93002 PRELIMINARY; PRT; 593 AA.
AC P93002; 004742;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE REGULATORY PROTEIN NPR1.
GN NPR1 OR NIM1.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC CAPPARALES; CRUCIFERAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOTYPE COLUMBIA;
RX MEDLINE; 97148688.
RA CAO H., GLAZEBROOK J., CLARKE J.D., VOLKO S., DONG X.;
RL CELL 88:57-63 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA RYALS J., WEYMANN K., LAWTON K., FRIEDRICH L., ELLIS D., STEINER H.Y.,
RA JOHNSON J., DELANEY T.P., JESSE T., VOS P., UKNES S.;
RL PLANT CELL 9:0-0(0).
DR EMBL; U76707; G1773295; -.
DR EMBL; U87794; G1916912; -.
SQ SEQUENCE 593 AA; 66031 MW; 1BE1666B CRC32;

Query Match 53.1%; Score 2184; DB 8; Length 593;
Best Local Similarity 51.2%; Pred. No. 0.00e+00;
Matches 307; Conservative 150; Mismatches 123; Indels 20; Gaps 14;

Db 1 MDTTIDGFADSYEISSTSFVATDNTDSSIVYLAEEQVLTGPDVSALQLLSNSFESVFD-S 59
|| : : : || : || : : | : : : : | : : : : | : : : : | : : : | : | : | : |
Qy 1 MDNSRTAFSDSNDISGSSSICCIGGGMTE-FFSPE-T-SPAEITSLKRLSETLESIFDAS 57
Db 60 -PD-DFYSDAKLVLSDG-REVSFHRCVLSARSSFFKSALAAKKEKDSNNNTAAVKLELKE 116
| : | : : | | | | : | : | : | | | | : | : | : | : | : | : | : |
Qy 58 LPEFDYFADAKLVSAGPCKEIPVHRCILSARSPFFKN-LFCGKKEKNS---S-KVELKE 111
Db 117 IAKDYEVGFDVVTVLAVYSSRVRPPPCKVSECADENCCHVACRPAVDFMLEVLYLAFI 176
: | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : |
Qy 112 VMKEHEVSYDAVMSVLAYLYSGKVRPSPKDVCVCVDNDCSHVACRPAVAFLVEVLYTSFT 171
Db 177 FKIPELITLYQRHLLDVVKVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDMVS 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 172 FQISELVDKFQRHLLDILDKTAADDVMMVLSVANICGKACERLLSSCIEIIIVKSNVDIIT 231
Db 237 LEKSLPEELVKEIIDRRKELGLEVPVK---KHVSNVHKALDSDDIELVKLLLKEDHTN 292
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 232 LDKALPHDIVKQITDSRAELGLQGPESNGFPDKHVKRIHRALDSDDVELLQMLLREGHTT 291
Db 293 LDDACALHFAVAYCNVKTATDLLKLDLADVNHRNPRGYTVLHVAAMRKEPQLILSLLKG 352
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 292 LDDAYALHYAVAYCDAKTTAELLDLALADINHQNSRGYTVLHVAAMRKEPKIVVSLLTKG 351

Db	353	ASASEATLEGR TALMI AKQATMAVE CNNIPEQCKHSLKGRLCVEILEQEDKREQIPRDVP	412
		: : : : : : : : : : : : : :	
Qy	352	ARPSDLTSDGRKALQIAKRLTRLVDFS KSPEEGKSASNDRLCIEILEQAERRDPLLGEAS	411
Db	413	PSFAVAADELKMTLLDLENRVALAQRLFPTEAQAA MEIAEMKGTCEFIVTSLEPDRLTGT	472
		: : : : : : : : : : :	
Qy	412	VSLAMAGDDL R MKLLYLENR VGLAKLLFPMEA KVAMDIAQVDGTSEFPLASIG-KKMANA	470
Db	473	KRTSPGVKIA PFRILEEHQSRLKALSKTVELGKRFFPRCSA VLDQIMNCEDLTQLACGED	532
		: : : : :	
Qy	471	QRTTVDLNEAPFKIKEEHLNRLRAL SRTVELGKRFFPRCSEVLN KIMDADDLSEIAYMGN	530
Db	533	DTAEKRLQKKQRYMEIQETLKKA FSEDNLELGNSSLTDSTSSTS KSTGGKRSNRKLSHRR	592
		: : : :	
Qy	531	DTAEERQLKKQRYMELQEILTKAFTEDKEEYDKTN-NI SSSCSTS KGVDKPN-KLPFRK	588



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Oct 5 10:59:59 1998; MasPar time 16.09 Seconds
591.174 Million cell updates/sec

Tabular output not generated.

Title: >US-08-908-884-14
Description: (1-588) from US08908884.pep
Perfect Score: 4115
Sequence: 1 MDNSRTAFSDSNDISGSSSI.....SSCSSTSKGVDKPNKLPFRK 588

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 36.213; Variance 178.711; scale 0.203

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	Pred. No.
	No.	Score	Match	Length		

1	2184	53.1	593	29	W23963	Arabidopsis thaliana	3.65e-174
2	172	4.2	991	16	R80096	Black widow spider de	5.09e-04
3	172	4.2	1214	16	R80097	Black widow spider de	5.09e-04
4	134	3.3	553	23	W15103	Myxoma virus MA55 gen	2.45e-01
5	117	2.8	226	21	W15483	Human P28.	3.38e+00
6	116	2.8	251	25	W05386	Mouse SH3P2 protein.	3.93e+00
7	112	2.7	943	10	R51499	Cyanobacteria replica	7.17e+00
8	105	2.6	231	9	R43385	Product of homeotic g	2.01e+01
9	105	2.6	394	22	W17845	Cytosolic phospholipa	2.01e+01
10	105	2.6	687	22	W17847	Cytosolic phospholipa	2.01e+01
11	105	2.6	688	22	W17848	Cytosolic phospholipa	2.01e+01
12	106	2.6	969	7	R33213	Sequence of the p105	1.74e+01
13	105	2.6	1078	6	R28963	Notch hN3k full lengt	2.01e+01
14	104	2.5	589	16	R94389	Mouse neural cell pro	2.33e+01
15	104	2.5	589	16	R94386	Human neural cell pro	2.33e+01
16	103	2.5	718	22	W01537	Bovine ribonuclease L	2.69e+01
17	104	2.5	752	17	R83018	Calcium-independent c	2.33e+01
18	104	2.5	752	20	W01479	Calcium-independent c	2.33e+01
19	104	2.5	752	22	W17849	Hamster cytosolic pho	2.33e+01
20	104	2.5	752	21	W13163	Ca-independent phosph	2.33e+01
21	98	2.4	229	25	W05403	Human clone 5 protein	5.51e+01
22	97	2.4	318	20	W06318	Human mitogen-activat	6.34e+01
23	97	2.4	657	6	R28964	Notch hN5k full lengt	6.34e+01
24	98	2.4	955	8	R42249	Human p50 protein DNA	5.51e+01
25	98	2.4	955	8	R42237	Human p50 protein DNA	5.51e+01
26	98	2.4	955	8	R42253	Human p50 protein DNA	5.51e+01
27	98	2.4	955	8	R42251	Human p50 protein DNA	5.51e+01
28	98	2.4	955	8	R42236	Human p50 protein DNA	5.51e+01
29	98	2.4	955	8	R42252	Human p50 protein DNA	5.51e+01
30	98	2.4	955	8	R42239	Human p50 protein DNA	5.51e+01
31	98	2.4	955	8	R42246	Human p50 protein DNA	5.51e+01
32	98	2.4	955	8	R42234	Human p50 protein DNA	5.51e+01
33	98	2.4	955	8	R42238	Human p50 protein DNA	5.51e+01
34	98	2.4	955	8	R42241	Human p50 protein DNA	5.51e+01
35	98	2.4	955	8	R42242	Human p50 protein DNA	5.51e+01
36	98	2.4	955	8	R42088	Human p50 or KBF1 pro	5.51e+01
37	98	2.4	955	8	R42250	Human p50 protein DNA	5.51e+01
38	98	2.4	955	8	R42240	Human p50 protein DNA	5.51e+01
39	98	2.4	955	8	R42245	Human p50 protein DNA	5.51e+01
40	98	2.4	955	8	R42247	Human p50 protein DNA	5.51e+01
41	98	2.4	955	8	R42244	Human p50 protein DNA	5.51e+01
42	98	2.4	955	8	R42243	Human p50 protein DNA	5.51e+01
43	98	2.4	955	8	R42235	Human p50 protein DNA	5.51e+01
44	98	2.4	955	8	R42248	Human p50 protein DNA	5.51e+01
45	96	2.3	422	21	W10693	Homology vector 443-8	7.31e+01

ALIGNMENTS

RESULT 1
ID W23963 standard; Protein; 593 AA.
AC W23963;
DT 17-JUN-1998 (first entry)

DE Arabidopsis thaliana NIM1 protein.
KW NIM1; noninducible immunity; disease resistance; plants;
KW SAR gene expression.
OS Arabidopsis thaliana.
PN WO9749822-A1.
PD 31-DEC-1997.
PF 10-MAR-1997; E01218.
PR 10-JAN-1997; US-035022.
PR 21-JUN-1996; US-020272.
PR 30-AUG-1996; US-024883.
PR 13-DEC-1996; US-033177.
PR 27-DEC-1996; US-773559.
PA (NOVS) NOVARTIS AG.
PI Delaney TP, Ellis DM, Friedrich LB, Johnson JE,
PI Lawton KA, Ryals JA, Weymann K;
DR WPI; 98-077185/07.
DR N-PSDB; V04632.
PT NIM1 gene which allows activation in plant of systemic acquired
PT resistance - useful to confer broad spectrum disease resistance in
PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and
PT corn
PS Disclosure; Fig 15; 153pp; English.
CC The sequence is that of the NIM1 (noninducible immunity) protein. It
CC may be used to confer a broad spectrum disease resistance in plants,
CC specifically crop plants, e.g. rice, wheat, barley, rye and corn.
CC The NIM1 gene can be used to confer universal disease susceptibility
CC to plant cells, and their progeny. It can also be used in a screening
CC method for identifying compounds capable of inducing broad spectrum
CC disease resistance in plants, while the plant cells, and their
CC progeny, can be used to isolate a gene fragment which allows
CC expression of broad spectrum disease resistance in plants, or to
CC incorporate the resistant trait into plant lines through breeding.
SQ Sequence 593 AA;

Query Match 53.1%; Score 2184; DB 29; Length 593;
Best Local Similarity 51.2%; Pred. No. 3.65e-174;
Matches 307; Conservative 150; Mismatches 123; Indels 20; Gaps 14;

Db 237 lekslpeelvkeiidrrkelglevpkvk----khvsnvhkaldsddielvkllkedhtn 292
|:|:|| ::||:| | | ||||:| : | ||| :||| ||||:||: :||:| |||
Qy 232 LDKALPHDIVKQITDSRAELGLQGPESNGFPDKHVKRIHRALDSDDVELLQMLLREGHTT 291

Db 293 lddacalhfavaycnvktatdlkldladvnhrnprgytvlhvaamrkepqlilsllekg 352
||||| |||:|||||: |||::|| | | ||||:||:||| |||:||| :||| |||
Qy 292 LDDAYALHYAVAYCDAKTTAELLDLALADINHQNSRGYTVLHVAAMRKEPKIVVSLTKG 351

Db 353 asaseatlegrtalmiakqatmavecnnipeqckhs1kgrlcveileqedkreqiprdvp 412
| :|: | :|| | |||: | | :|: | : : | |||:||| :||: : : :
Qy 352 ARPSDLTSDGRKALQIAKRLTRLVDFSKSPEEGKSASNDRLCIEILEQAERRDPLLGEAS 411

Db 413 psfavaadelkmtlldlenrvlaqrlfpteaqaaameiaemkgtcefivtslepdrltgt 472
|:|:|:|:|:| | | ||||:|| | ||| ||| |||:||: | ||| :||: : : :
Qy 412 VSLAMAGDDLRLMKLLYLENRVGLAKLLFPMEAKVAMDIAQVDGTSEFPLASIG-KKMANA 470

Db 473 krtspgvkiapfrileehqsrlkalsktvelgkrffprcsavldqimncedltqlacged 532
||: : | |||:| | | :||:||:|||:||| ||| ||| |||:||: | ||: :||:|| :
Qy 471 QRTTVDLNEAPFKIKEEHLNRLRALSRTVELGKRFFPRCSEVLNKIMDADDLSEIAYMGN 530

Db 533 dtaekrlqkkqrymeiqetlkkafsednlegnssltdstsstskstggkrsnrklshrr 592
||||| | | ||||:|| | |||:||: | ::: | :| : | | :|| | :| :| :
Qy 531 DTAEERQLKKQRYMELQEILTKAFTEDKEEYDKTN-NISSLCSSTSKGVDKPN-KLPFRK 588